























```

Query Match
Post Local Statistics: 1999-08-06
Number of Seqs to Test: 41
Sequences Found: 174
Matches: 414
Seq ID No. 1
Length: 450
CYP11B
ORGANISM: Mus musculus A.M.M.10
FEATURES
NAME/KEY: M.10.BES
Location: (114)
OTHER INFORMATION: Xaa = H
NAME/KEY: M.10.BES
Location: (114)
OTHER INFORMATION: Xaa = A
OTHER INFORMATION: Xaa = A
Query Match
Post Local Statistics: 1999-08-06
Number of Seqs to Test: 41
Sequences Found: 174
Matches: 414
Seq ID No. 1
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ORGANISM: Mus musculus A.M.M.10
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Location: (114)
OTHER INFORMATION: Xaa = H
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Location: (114)
OTHER INFORMATION: Xaa = A
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Query Match
Post Local Statistics: 1999-08-06
Number of Seqs to Test: 41
Sequences Found: 174
Matches: 414
Seq ID No. 1
Length: 450
CYP11B
ORGANISM: Mus musculus A.M.M.10
FEATURES
NAME/KEY: M.10.BES
Location: (114)
OTHER INFORMATION: Xaa = H
NAME/KEY: M.10.BES
Location: (114)
OTHER INFORMATION: Xaa = A
OTHER INFORMATION: Xaa = A

```













GenCore version 5.1.3  
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M program: Protein search, using SW model

Parameters: November 16, 2002, 16:25:41 : Search time 49 Seconds  
(without alignment)  
4442.368 M lion cell updates/secDatabase: MS7062  
Gapop 10.0, Gapext 0.5  
Sequences: 1104  
MS 7062 469-2  
Protein search: 1104  
Sequences: 1104

Method: 44580 seqs, 20804715 residues

Total number of hits satisfying chosen parameters: 67586

Maximum hit seq length: 208000000

Post processed: Minimum Match: 0.8  
Maximum Match: 100%

Listing first 45 summaries

Hit name: 1: SPKPMH\_21:\*

2: SP\_01001:\*

3: SP\_01001:\*

4: SP\_01001:\*

5: SP\_01001:\*

6: SP\_01001:\*

7: SP\_01001:\*

8: SP\_01001:\*

9: SP\_01001:\*

10: SP\_01001:\*

11: SP\_01001:\*

12: SP\_01001:\*

13: SP\_01001:\*

14: SP\_01001:\*

15: SP\_01001:\*

16: SP\_01001:\*

17: SP\_01001:\*

Prod. N. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is divided by analysis of the total score distribution.

## SUMMARIES

Result N.	Score	Match Length DB	ID	Description
1	17.5	1072	4	CHIE57 homo sapien
2	17.5	1061	4	CHIE57 homo sapien
3	17.5	1061	4	CHIE57 homo sapien
4	17.5	1061	4	CHIE57 homo sapien
5	17.5	1061	4	CHIE57 homo sapien
6	17.5	1061	4	CHIE57 homo sapien
7	17.5	1061	4	CHIE57 homo sapien
8	17.5	1061	4	CHIE57 homo sapien
9	17.5	1061	4	CHIE57 homo sapien
10	17.5	1061	4	CHIE57 homo sapien
11	17.5	1061	4	CHIE57 homo sapien
12	17.5	1061	4	CHIE57 homo sapien
13	17.5	1061	4	CHIE57 homo sapien
14	17.5	1061	4	CHIE57 homo sapien
15	17.5	1061	4	CHIE57 homo sapien
16	17.5	1061	4	CHIE57 homo sapien
17	17.5	1061	4	CHIE57 homo sapien
18	17.5	1061	4	CHIE57 homo sapien
19	17.5	1061	4	CHIE57 homo sapien
20	17.5	1061	4	CHIE57 homo sapien
21	17.5	1061	4	CHIE57 homo sapien
22	17.5	1061	4	CHIE57 homo sapien
23	17.5	1061	4	CHIE57 homo sapien
24	17.5	1061	4	CHIE57 homo sapien
25	17.5	1061	4	CHIE57 homo sapien
26	17.5	1061	4	CHIE57 homo sapien
27	17.5	1061	4	CHIE57 homo sapien
28	17.5	1061	4	CHIE57 homo sapien
29	17.5	1061	4	CHIE57 homo sapien
30	17.5	1061	4	CHIE57 homo sapien
31	17.5	1061	4	CHIE57 homo sapien
32	17.5	1061	4	CHIE57 homo sapien
33	17.5	1061	4	CHIE57 homo sapien
34	17.5	1061	4	CHIE57 homo sapien
35	17.5	1061	4	CHIE57 homo sapien
36	17.5	1061	4	CHIE57 homo sapien
37	17.5	1061	4	CHIE57 homo sapien
38	17.5	1061	4	CHIE57 homo sapien
39	17.5	1061	4	CHIE57 homo sapien
40	17.5	1061	4	CHIE57 homo sapien
41	17.5	1061	4	CHIE57 homo sapien
42	17.5	1061	4	CHIE57 homo sapien
43	17.5	1061	4	CHIE57 homo sapien
44	17.5	1061	4	CHIE57 homo sapien
45	17.5	1061	4	CHIE57 homo sapien

17	97.5	1061	4	CHIE57
18	97.5	1061	4	CHIE57
19	97.5	1061	4	CHIE57
20	97.5	1061	4	CHIE57
21	97.5	1061	4	CHIE57
22	97.5	1061	4	CHIE57
23	97.5	1061	4	CHIE57
24	97.5	1061	4	CHIE57
25	97.5	1061	4	CHIE57
26	97.5	1061	4	CHIE57
27	97.5	1061	4	CHIE57
28	97.5	1061	4	CHIE57
29	97.5	1061	4	CHIE57
30	97.5	1061	4	CHIE57
31	97.5	1061	4	CHIE57
32	97.5	1061	4	CHIE57
33	97.5	1061	4	CHIE57
34	97.5	1061	4	CHIE57
35	97.5	1061	4	CHIE57
36	97.5	1061	4	CHIE57
37	97.5	1061	4	CHIE57
38	97.5	1061	4	CHIE57
39	97.5	1061	4	CHIE57
40	97.5	1061	4	CHIE57
41	97.5	1061	4	CHIE57
42	97.5	1061	4	CHIE57
43	97.5	1061	4	CHIE57
44	97.5	1061	4	CHIE57
45	97.5	1061	4	CHIE57

A: 100%

ALPHA-5

17	97.5	1061	4	CHIE57
18	97.5	1061	4	CHIE57
19	97.5	1061	4	CHIE57
20	97.5	1061	4	CHIE57
21	97.5	1061	4	CHIE57
22	97.5	1061	4	CHIE57
23	97.5	1061	4	CHIE57
24	97.5	1061	4	CHIE57
25	97.5	1061	4	CHIE57
26	97.5	1061	4	CHIE57
27	97.5	1061	4	CHIE57
28	97.5	1061	4	CHIE57
29	97.5	1061	4	CHIE57
30	97.5	1061	4	CHIE57
31	97.5	1061	4	CHIE57
32	97.5	1061	4	CHIE57
33	97.5	1061	4	CHIE57
34	97.5	1061	4	CHIE57
35	97.5	1061	4	CHIE57
36	97.5	1061	4	CHIE57
37	97.5	1061	4	CHIE57
38	97.5	1061	4	CHIE57
39	97.5	1061	4	CHIE57
40	97.5	1061	4	CHIE57
41	97.5	1061	4	CHIE57
42	97.5	1061	4	CHIE57
43	97.5	1061	4	CHIE57
44	97.5	1061	4	CHIE57
45	97.5	1061	4	CHIE57



































entity Match: 25.08; score 1525; len 1; length 997;

1.  $\mathcal{L} = \mathcal{L}_1 \cup \mathcal{L}_2$  and  $\mathcal{L}_1 \cap \mathcal{L}_2 = \emptyset$ .

















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EM protein: protein search, using SW model

Parameters: December 16, 2002, 16:25:40 : Search time 2h 56m 5s  
(without a liquidus)  
4682015 Million cell updates/sec

EM protein: protein search, using SW model

Parameters: December 16, 2002, 16:25:40 : Search time 2h 56m 5s  
(without a liquidus)  
4682015 Million cell updates/sec

EM protein: protein search, using SW model

Parameters: December 16, 2002, 16:25:40 : Search time 2h 56m 5s  
(without a liquidus)  
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EM protein: protein search, using SW model

Parameters: December 16, 2002, 16:25:40 : Search time 2h 56m 5s  
(without a liquidus)  
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EM protein: protein search, using SW model

Parameters: December 16, 2002, 16:25:40 : Search time 2h 56m 5s  
(without a liquidus)  
4682015 Million cell updates/sec

EM protein: protein search, using SW model

Parameters: December 16, 2002, 16:25:40 : Search time 2h 56m 5s  
(without a liquidus)  
4682015 Million cell updates/sec

EM protein: protein search, using SW model

# SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	144.5	28.5	1295	2	T18517	procollagen N-endo
2	144.5	22.1	2165	2	T21371	gene ADAMTS-1 prot
3	129.5	21.2	951	2	T00017	hypothetical prote
4	109.5	18.0	837	2	T00355	hypothetical prote
5	83.5	14.0	550	2	T47158	hypothetical prote
6	82.4	14.5	1558	2	C89114	protein C17C3.6a.1
7	82.4	14.5	2167	2	T134395	hypothetical prote
8	70.5	11.6	1444	2	T18856	angiogenesis inhib
9	64.4	10.9	951	2	T00260	hypothetical prote
10	56.3	9.6	850	2	T16892	hypothetical prote
11	53.9	8.7	1059	2	T22545	hypothetical prote
12	46.4	7.5	957	2	T15976	hypothetical prote
13	45.3	7.3	836	2	A00000	hypothetical prote
14	41.3	6.9	903	2	S60257	melanin alpha - mu
15	39.9	6.5	898	2	T14764	hypothetical prote
16	38.7	6.3	617	2	S48160	metalloproteinase
17	37.5	6.2	414	2	T02390	disintegrin-like m
18	37.5	5.9	909	2	S55270	cathepsin B
19	36.5	5.8	549	2	S48169	metalloproteinase
20	35.3	5.4	421	1	HYSN8A	librolase (EC 3.4.
21	34.3	5.2	571	2	S24789	librolase (EC 3.4.
22	33.5	5.2	610	2	J07530	cathepsin B
23	33.5	5.2	610	2	J07530	cathepsin B
24	31.5	5.4	478	2	J04880	cathepsin B
25	31.5	5.4	478	2	J04880	cathepsin B
26	31.5	5.4	478	2	J04880	cathepsin B
27	31.5	5.4	478	2	J04880	cathepsin B
28	31.5	5.4	478	2	J04880	cathepsin B
29	31.5	5.4	478	2	J04880	cathepsin B

40	30.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
41	30.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
42	30.8	5.2	113	2	HYSN8A	librolase (EC 3.4.
43	30.6	5.2	113	2	HYSN8A	librolase (EC 3.4.
44	30.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
45	30.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
46	29.7	5.2	113	2	HYSN8A	librolase (EC 3.4.
47	29.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
48	29.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
49	29.0	5.2	113	2	HYSN8A	librolase (EC 3.4.
50	28.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
51	28.8	5.2	113	2	HYSN8A	librolase (EC 3.4.
52	28.7	5.2	113	2	HYSN8A	librolase (EC 3.4.
53	28.6	5.2	113	2	HYSN8A	librolase (EC 3.4.
54	28.5	5.2	113	2	HYSN8A	librolase (EC 3.4.
55	28.4	5.2	113	2	HYSN8A	librolase (EC 3.4.
56	28.3	5.2	113	2	HYSN8A	librolase (EC 3.4.
57	28.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
58	28.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
59	28.0	5.2	113	2	HYSN8A	librolase (EC 3.4.
60	27.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
61	27.8	5.2	113	2	HYSN8A	librolase (EC 3.4.
62	27.7	5.2	113	2	HYSN8A	librolase (EC 3.4.
63	27.6	5.2	113	2	HYSN8A	librolase (EC 3.4.
64	27.5	5.2	113	2	HYSN8A	librolase (EC 3.4.
65	27.4	5.2	113	2	HYSN8A	librolase (EC 3.4.
66	27.3	5.2	113	2	HYSN8A	librolase (EC 3.4.
67	27.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
68	27.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
69	27.0	5.2	113	2	HYSN8A	librolase (EC 3.4.
70	26.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
71	26.8	5.2	113	2	HYSN8A	librolase (EC 3.4.
72	26.7	5.2	113	2	HYSN8A	librolase (EC 3.4.
73	26.6	5.2	113	2	HYSN8A	librolase (EC 3.4.
74	26.5	5.2	113	2	HYSN8A	librolase (EC 3.4.
75	26.4	5.2	113	2	HYSN8A	librolase (EC 3.4.
76	26.3	5.2	113	2	HYSN8A	librolase (EC 3.4.
77	26.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
78	26.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
79	26.0	5.2	113	2	HYSN8A	librolase (EC 3.4.
80	25.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
81	25.8	5.2	113	2	HYSN8A	librolase (EC 3.4.
82	25.7	5.2	113	2	HYSN8A	librolase (EC 3.4.
83	25.6	5.2	113	2	HYSN8A	librolase (EC 3.4.
84	25.5	5.2	113	2	HYSN8A	librolase (EC 3.4.
85	25.4	5.2	113	2	HYSN8A	librolase (EC 3.4.
86	25.3	5.2	113	2	HYSN8A	librolase (EC 3.4.
87	25.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
88	25.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
89	25.0	5.2	113	2	HYSN8A	librolase (EC 3.4.
90	24.9	5.2	113	2	HYSN8A	librolase (EC 3.4.
91	24.8	5.2	113	2	HYSN8A	librolase (EC 3.4.
92	24.7	5.2	113	2	HYSN8A	librolase (EC 3.4.
93	24.6	5.2	113	2	HYSN8A	librolase (EC 3.4.
94	24.5	5.2	113	2	HYSN8A	librolase (EC 3.4.
95	24.4	5.2	113	2	HYSN8A	librolase (EC 3.4.
96	24.3	5.2	113	2	HYSN8A	librolase (EC 3.4.
97	24.2	5.2	113	2	HYSN8A	librolase (EC 3.4.
98	24.1	5.2	113	2	HYSN8A	librolase (EC 3.4.
99	24.0	5.2	113	2	HYSN8A	librolase (EC 3.4.
100	23.9	5.2	113	2	HYSN8A	librolase (EC 3.4.



[illegible]





[illegible]



964 SGGTSS TGGG HKKVCKSAHRA LIPAHSAKAPALMKNLKKCPARWAGDHO 1013  
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576 SGGTSS TGGG HKKVCKSAHRA LIPAHSAKAPALMKNLKKCPARWAGDHO 1013  
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Search completed on 12/18/2002 at 10:54:26  
 Job time: 34 seconds































GenCorp version 5.1.3  
Copyright (c) 1993 - 2002 Computer Ltd.

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

(without alignment)

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

# SUMMARIES

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

Search results using frame\_plus.p2n mode

5	5915.5	1	AX12776
6	5742	2	AX12776
7	5742	3	AX12776
8	5742.5	4	AX12776
9	5675	5	AX12776
10	5675	6	AX12776
11	5675	7	AX12776
12	5675	8	AX12776
13	5675	9	AX12776
14	5675	10	AX12776
15	5675	11	AX12776
16	5675	12	AX12776
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18	5675	14	AX12776
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21	5675	17	AX12776
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41	5675	37	AX12776
42	5675	38	AX12776
43	5675	39	AX12776
44	5675	40	AX12776
45	5675	41	AX12776

ALIGNMENT

RESULT 1	
ES5273	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

Search results using frame\_plus.p2n mode







[illegible][illegible]











[illegible][illegible]

Donna Scharf, Rebecca Chavkin, Patricia Vetter, and Elizabeth K. Kopp, eds., *Practical Pathways: Building a Better Tomorrow*. Baltimore, Edith Lewis Publishing, 2005. Pp. 208. \$24.95.

Kaplan, Lieberman, R., Cook, W.J., and Silos-Santafé, L. (1992), "Human metallothionein family member and uses: Patent: WO 018156 A 10-22-NOV-2001," *International Pharmaceutical*, Inc. (this).



[illegible][illegible]





















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743 AspValValTrpIleProLysGlySerValHisIlePheIleValAspLeuAspLeuSer 742







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RESULT:

US-09-842-469-2 (1-11-04) x US-09-369-364A-14 (1-26-25)

SEQUENCE: 14 Affected: 05/09/09/06/1A

1. Patient Name: 09/06/1A

2. Patient ID: 09/06/1A

3. Patient Name: 09/06/1A

4. Patient Name: 09/06/1A

5. Patient Name: 09/06/1A

6. Patient Name: 09/06/1A

7. Patient Name: 09/06/1A

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463. Patient Name: 09/06/1A

[illegible]

Job time : 2'42 sec's

Received: December 17, 2002, 07:09:08

Scenoco version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

Model: Scenario search, using framePlus.rgn model  
Run: 17, 2002, 06:13:42 : Search time 487 Seconds  
(without alignment)  
510,146 Million cell updates/sec

Score: 442,469.2

IC: 5000.2  
Xapopt: 0.5  
Yapopt: 0.5  
Popt: 7.0  
Japopt: 7.0

Score: 218,239.959, 112,599,159 residues

Initial number of cells satisfying chosen parameters: 4,704,78

Maximum hit score: 200000000

Maximum hit score location: 200000000

Maximum Match: 100%

Initial First 45 summaries

Model: Scenario search, using framePlus.rgn model  
Run: 17, 2002, 06:13:42 : Search time 487 Seconds  
(without alignment)  
510,146 Million cell updates/sec  
Score: 442,469.2  
IC: 5000.2  
Xapopt: 0.5  
Yapopt: 0.5  
Popt: 7.0  
Japopt: 7.0  
Score: 218,239.959, 112,599,159 residues  
Initial number of cells satisfying chosen parameters: 4,704,78  
Maximum hit score: 200000000  
Maximum hit score location: 200000000  
Maximum Match: 100%  
Initial First 45 summaries

Model: Scenario search, using framePlus.rgn model

Model: Scenario search, using framePlus.rgn model  
Run: 17, 2002, 06:13:42 : Search time 487 Seconds  
(without alignment)  
510,146 Million cell updates/sec  
Score: 442,469.2  
IC: 5000.2  
Xapopt: 0.5  
Yapopt: 0.5  
Popt: 7.0  
Japopt: 7.0  
Score: 218,239.959, 112,599,159 residues  
Initial number of cells satisfying chosen parameters: 4,704,78  
Maximum hit score: 200000000  
Maximum hit score location: 200000000  
Maximum Match: 100%  
Initial First 45 summaries

Print: No. is the number of results predicted by scores to have a  
score greater than or equal to the score being printed,  
and is derived by analysis of the total score distribution.

100% Accepted  
Applicant -1  
For file -2

Result No.	Score	Match	Length	...
1	6096	...	...	...
2	6080.5	...	...	...
3	6076.5	...	...	...
4	6072.5	...	...	...
5	6028.5	...	...	...
6	5942	...	...	...
7	5942	...	...	...
8	5724.5	...	...	...
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[illegible][illegible]

[illegible][illegible]

















blast distribution. Most close distribution information can be found within the NCBI database. The following information is provided for the BLAST results: 51 rows in column 14. This table was selected for full length sequencing because it passed the following selection criteria: Exon frequency 60% and 75%.

This table has the following problems: no polyA tail.

## FEATURES

Source:

Location/Qualifiers

1-795

Accession: "Homo sapiens"

Accession: "Homo sapiens"

Accession: "Homo sapiens"

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Accession: "Homo sapiens"

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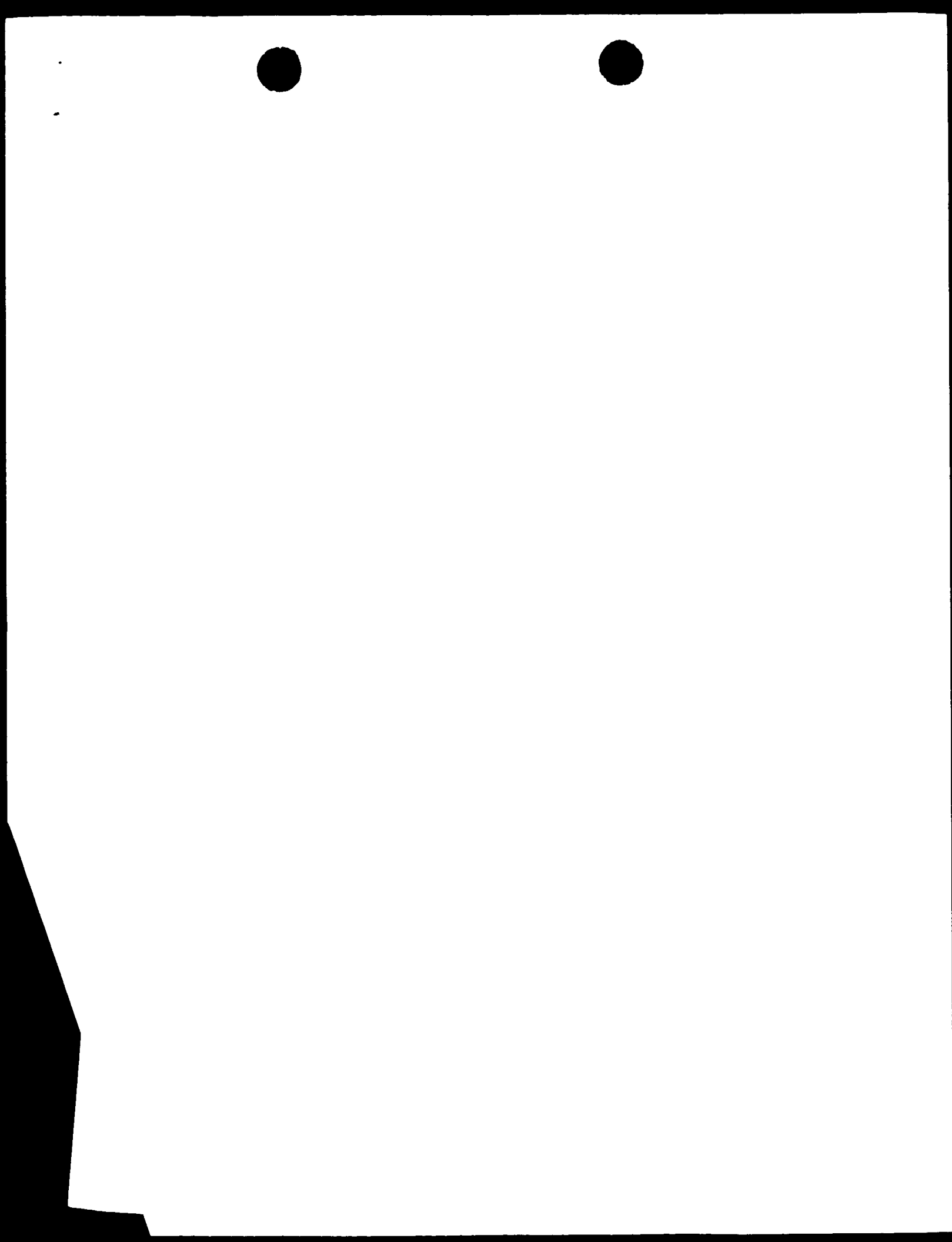




















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